

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=12; min=45; sec=12; ms=146;]

=====

Reviewer Comments:

Leu Glu Phe
30

Tyr Thr Lys Arg Leu Phe Gln Ser Val Ser Pro Ser Phe Leu Ser Ile
35 40 45

Please correct invalid amino acid numbering shown above in sequence id# 48. Please check the remaining sequences for similar errors.

Application No: 10785116 Version No: 3.0

Input Set:

Output Set:

Started: 2009-01-07 15:10:48.392
Finished: 2009-01-07 15:10:52.884
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 492 ms
Total Warnings: 33
Total Errors: 9
No. of SeqIDs Defined: 49
Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

Input Set:

Output Set:

Started: 2009-01-07 15:10:48.392
Finished: 2009-01-07 15:10:52.884
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 492 ms
Total Warnings: 33
Total Errors: 9
No. of SeqIDs Defined: 49
Actual SeqID Count: 49

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)
E 323	Invalid/missing amino acid numbering SEQID (48)at Protein (35)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (36)
E 323	Invalid/missing amino acid numbering SEQID (48)at Protein (40)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (41)
E 323	Invalid/missing amino acid numbering SEQID (48)at Protein (45)
E 323	Invalid/missing amino acid numbering SEQID (48) POS (46)

SEQUENCE LISTING

<110> Pecker, Iris
Vlodavsky , Israel
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME
IN GENETICALLY MODIFIED CELLS

<130> 27674

<140> 10785116

<141> 2004-02-25

<160> 49

<170> PatentIn version 3.1

<210> 1

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 1

ccatcctaatacgaactcactatagggc

27

<210> 2

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 2

gtagtgatgcacatgtaactgaatc

24

<210> 3

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 3

actcactatagggctcgagcggc

23

<210> 4

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 4

gcaccttagc cgtctttctt cg 22

<210> 5

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 5

tttttttttt ttttt 15

<210> 6

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 6

ttcgatccca agaaggaatc aac 23

<210> 7

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide

<400> 7

gtagtgatgc catgtaactg aatc 24

<210> 8

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Peptide derived from tryptic digestion of human heparenase

<400> 8

Tyr Gly Pro Asp Val Gly Gln Pro Arg

1 5

<210> 9
<211> 1721
<212> DNA
<213> Homo sapiens

<400> 9
ctagagcttt cgactctccg ctgcgcggca gctggcgggg ggagcagcca ggtgagccca 60

agatgctgct gcgctcgaag cctgcgctgc cgccgcgct gatgctgctg ctcttggggc 120

cgctgggtcc cctctcccct ggcgccctgc cccgacctgc gcaagcacag gacgtcgtgg 180

acctggactt cttcaccag gagccgctgc acctggtgag cccctcgttc ctgtccgtca 240

ccattgacgc caacctggcc acggaccgc ggttcctcat cctcctgggt tctccaaagc 300

ttcgtacctt ggccagaggc ttgtctcctg cgtacctgag gtttgggtggc accaagacag 360

acttcctaata tttcgatccc aagaaggaat caacctttga agagagaagt tactggcaat 420

ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tcctgatgtg gaggagaagt 480

tacggttgga atggccctac caggagcaat tgctactccg agaacactac cagaaaaagt 540

tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct 600

caggactgga cttgatcttt ggccataatg cgttattaag aacagcagat ttgcagtgga 660

acagttctaa tgctcagttg ctctggact actgctcttc caaggggtat aacatttctt 720

gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt 780

cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa 840

atgcaaaact ctatggtcct gatgttggtc agcctcgaag aaagacggct aagatgctga 900

agagcttcct gaaggctggg ggagaagtga ttgattcagt tacatggcat cactactatt 960

tgaatggacg gactgctacc aggaagatt ttctaaacct tgatgtattg gacattttta 1020

tttcatctgt gcaaaaagtt ttccaggtgg ttgagagcac caggcctggc aagaaggtct 1080

ggttaggaga aacaagctct gcatatggag gcggagcgcc cttgctatcc gacacctttg 1140

cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga atagaagtgg 1200

tgatgaggca agtattcttt ggagcaggaa actaccattt agtggatgaa aacttcgatc 1260

ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aaggtgttaa 1320

tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaaca 1380

ctgacaatcc aaggtataaa gaaggagatt taactctgta tgccataaac ctccataacg 1440

tcaccaagta cttgcgggta ccctatcctt tttctaaca gcaagtggat aaataccttc 1500

taagaccttt gggacctcat ggattacttt ccaaactctgt ccaactcaat ggtctaactc 1560
 taaagatggg ggatgatcaa accttgccac ctttaattgga aaaacctctc cggccaggaa 1620
 gttcactggg cttgccagct ttctcatata gtttttttgt gataagaaat gccaaagttg 1680
 ctgcttgcat ctgaaaataa aatatactag tcctgacact g 1721

<210> 10
 <211> 543
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 1 5 10 15

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
 35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
 100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
 115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
 130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
 145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
 165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
 180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
 195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
 210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
 225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
 245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
 260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
 275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
 290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
 305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
 325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
 340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
 355 360 365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
 370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
500 505 510

Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
515 520 525

Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
530 535 540

<210> 11
<211> 1721
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (63)..(1691)
<223>

<400> 11
ctagagcttt cgactctccg ctgcgcggca gctggcgggg ggagcagcca ggtgagccca 60

ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ccg ctg atg ctg 107
Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu

1	5	10	15	
ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga				155
Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg				
	20	25	30	
cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag				203
Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu				
	35	40	45	
ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc				251
Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala				
	50	55	60	
aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag				299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys				
	65	70	75	
ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt				347
Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly				
80	85	90	95	
ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc				395
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr				
	100	105	110	
ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc				443
Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys				
	115	120	125	
aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa				491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu				
	130	135	140	
tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag				539
Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys				
	145	150	155	
ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act				587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr				
160	165	170	175	
ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta				635
Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu				
	180	185	190	
tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc				683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu				
	195	200	205	
ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc				731
Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly				
	210	215	220	
aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg				779
Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly				
	225	230	235	

tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag	827
Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys	
240 245 250 255	
tcc acc ttc aaa aat gca aaa ctc tat ggt cct gat gtt ggt cag cct	875
Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro	
260 265 270	
cga aga aag acg gct aag atg ctg aag agc ttc ctg aag gct ggt gga	923
Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly	
275 280 285	
gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg	971
Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg	
290 295 300	
act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt	1019
Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe	
305 310 315	
att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct	1067
Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro	
320 325 330 335	
ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga	1115
Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly	
340 345 350	
gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat	1163
Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp	
355 360 365	
aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa	1211
Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln	
370 375 380	
gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat	1259
Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp	
385 390 395	
cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc	1307
Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly	
400 405 410 415	
acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt	1355
Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu	
420 425 430	
cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa	1403
Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu	
435 440 445	
gga gat tta act ctg tat gcc ata aac ctc cat aac gtc acc aag tac	1451
Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr	
450 455 460	

ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt	1499
Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu	
465 470 475	
cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc	1547
Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu	
480 485 490 495	
aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta	1595
Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu	
500 505 510	
atg gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc	1643
Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe	
515 520 525	
tca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc	1691
Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile	
530 535 540	
tgaaaataaaa atatactagt cctgacactg	1721

<210> 12
 <211> 824
 <212> DNA
 <213> Mus musculus

<400> 12	
ctggcaagaa ggtctgggtg ggagagacga gctcagctta cggtagcggt gcacccttgc	60
tgtccaacac ctttgcagct ggttttatgt ggctggataa attgggcctg tcagcccaga	120
tgggcataga agtcgtgatg aggcaggtgt tcttcggagc aggcaactac cacttagtgg	180
atgaaaactt tgagccttta cctgattact ggctctctct tctgttcaag aaactggtag	240
gtcccagggt gttactgtca agagtgaaag gccagacag gagcaaaactc cgagtgtatc	300
tccactgcac taacgtctat caccacgat atcaggaagg agatctaact ctgtatgtcc	360
tgaacctcca taatgtcacc aagcacttga aggtaccgcc tccgttggtc aggaaaccag	420
tggatacgta ccttctgaag ccttcggggc cggatggatt actttccaaa tctgtccaac	480
tgaacggtca aattctgaag atggtggatg agcagaccct gccagctttg acagaaaaac	540
ctctccccgc aggaagtgca ctaagcctgc ctgccttttc ctatggtttt tttgtcataa	600
gaaatgccaa aatcgctgct tgtatatgaa aataaaaggc atacgtacc cct	